IN THE SPECIFICATION:

On page 9, lines 25-27, please amend the paragraph as follows:

FIG. 3 ~~despicts~~ depicts the nucleotide (SEQ ID NOs 71-72) and amino acid (SEQ ID NO 73) sequences of the synthetic fragment K2. The two phosphorylation sites recognized by the cAMP-dependent protein kinase is underlined. The cloning site, XmaI, is shown in italics.

On page 15, lines 7-11, please amend the paragraph as follows:

FIG. 38 is a comparison of primary sequences of MAb-chCC49, MAb231 and MAb61.1.3 in the hinge region. A: Primary sequences of MAb-chCC49 (SEQ ID NO. 74), MAb231 (SEQ ID NO. 75) and MAb61.1.3 (SEQ ID NO. 76) in the hinge region are aligned. B: Bestfit of primary sequence of MAb-chCC49 (SEQ ID NO. 74) to that of MAb231 (SEQ ID NO. 75) in the hinge region. C: Bestfit of primary sequence MAb-chCC49 (SEQ ID NO. 74) to that of MAb61.1.3 (SEQ ID NO. 76) in the hinge region.

On page 62, lines 5-20, please amend the paragraph as follows:

By following the first criterium, twelve sites in the whole MAb-chCC49 molecule were found for introduction of PKA site. Evaluation of 3D models of these putative mutant Abs and model of MAb-chCC49 suggested that not all these sites were good for site-directed mutagenesis (Table 8) (SEQ ID NOs 47-70). First, analysis of the MAb-chCC49 model revealed that four out of twelve potential sites (site 5, 6, 8, 9) were buried. Furthermore, it was showed by molecular modeling that introduction of arginine residues into these sites would cause severe steric problems in the structure of the MAb-chCC49 molecule (Table 8). These sites, therefore, were excluded for further consideration. The rest of the sites were examined to see if the mutations of the sites would change the CDR regions of MAb-chCC49 as described. Site 11 was excluded since all four amino acid residues in the PKA recognition site are in the CDR2 region of the light chains of MAb-chCC49. Mutations of some amino acid residues (*e.g.* Cys320 in site 6, and Pro117 in site 12) were also avoided since these residues might play critical roles in maintaining

proper structure of the MAb. Those possible mutants, which did not show the obvious problems of the above kinds, were eventually chosen (three sites on the heavy chain and one site on the light chain) for the further work.

SEQUENCE LISTING:

Please replace the originally filed Sequence Listing with the enclosed substitute Sequence Listing.